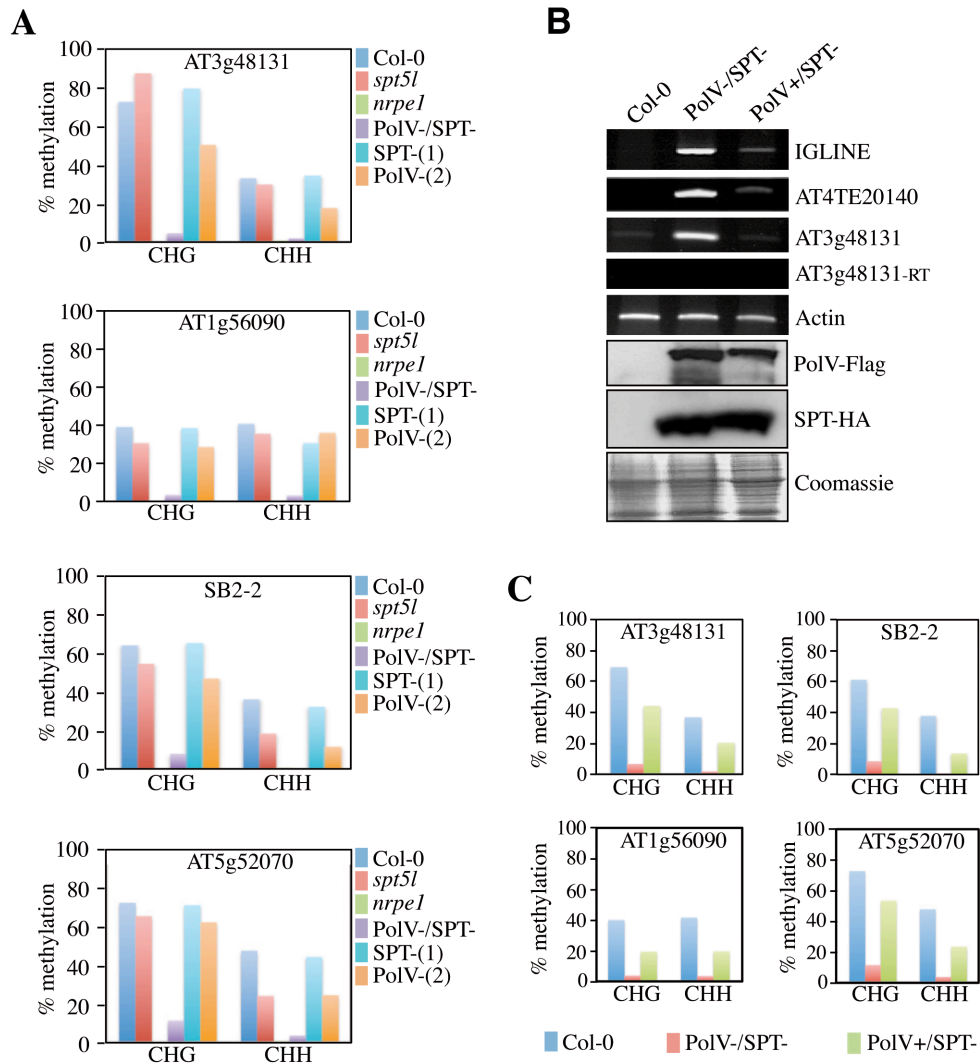


Supplemental\_Fig\_S3



**Supplemental Fig.S3: Methylation analysis of RdDM targets.**

A) Analysis of DNA methylation by bisulfite sequencing in CHG and CHH contexts at four RdDM targets (namely AT3g48131, SB2-2, AT1g56090 and AT5g52070) in wild-type (Col-0), *nrpe1*, *spt5l*, PolV-/SPT- cross line and two SPT-(1) and PolV-(2) complemented lines. B) *Top panel*: Transcript level analysis by RT PCR at RdDM targets in Col-0, PolV-/SPT- and PolV+/SPT- cross lines. *ACTIN2* is used as a loading control and –RT reactions are used to assess genomic DNA contamination. *Bottom panel*: Detection of NRPE1 and SPT5L variants by western blots in the crosses lines. NRPE1 and SPT5L variants were detected respectively with anti-Flag and anti-HA antibodies. Coomassie blue staining indicates equal loading. C) Analysis of DNA methylation by bisulfite sequencing in CHG and CHH contexts at 4 RdDM targets in Col-0, and the PolV-/SPT- and PolV+/SPT- cross lines.